

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Role, Lorna W.
- (ii) TITLE OF INVENTION: SPLICE VARIANTS OF THE HEREGULIN GENE,  
nARIA,  
AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Cooper & Dunham LLP
  - (B) STREET: 1185 Avenue of the Americas
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: White, John P.
  - (B) REGISTRATION NUMBER: 28,678
  - (C) REFERENCE/DOCKET NUMBER: 46839-A
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 212-278-0400
  - (B) TELEFAX: 212-391-0526

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3212 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGATGCTGC TGCTACTGTC ACTTCTGCCG CTGCCGCTGT TGTACAGAT TTTGCTTTTG  
60  
CTCCTTCTAC CGCATGACAA TTGTTTTCTT CGCCTAAGCA GATACCAGCC TCAGATGCTC  
120  
AAGGTGAGAG TCTTGCCTTT CGCTCTGGGC TATTGGTTCA CTTAATCCGG TCAATTTGTT  
180  
CGCTGCTCGT GGTGTCTTT CTCCCCGCC TCCTTCCCC TGTTTTGTTT TGTTTCGCTT  
240  
GCTTTCGGGG GGACGCTCCT TCCCTCAGTC AGAAGAGCTG GAATTGCTTG AGAGGCGTAT  
300  
AAGGAATTAT AAAAGTGGCC AGGAAACACG AGCGCAGTGA CTGCAGAGCT GCCCTTGGCT  
360  
TCGGCAAGGC AGCGTGAGCG GCAGAGGGCT CGGGCAGGGG GCGGGGGGTC TCCTTTTTCC  
420  
CGTGCGTTCC TCTTCTCCA GTTCGATGA TGTGCTGTT TCGGACCTCT CGCTGACTCC  
480  
TGCCCTGTGA TTTTGCTGA GCGCTGTGAC TGTTACTCCG TCTCTTTCTG TCTGTGTTTC  
540  
ACAGTAATGG ACTGTGATAG AGTTAAGGCC TTTTGGAGGT GAGCTGTGTC ACAGCTGATG  
600  
CTTAAACATG TCTGAAGTAG GCACCGAGAC TTTCCCCAGC CCCTCGGCTC AGCTGAGCCC  
660  
TGATGCATCC CTTGGGGGGC TCCCGGCTGA GGAGAACATG CCGGGGCCCC ACAGAGAGGA  
720  
CAGCAGGGTC CCAGGTGTGG CAGGCCTGGC CTCGACCTGC TCGTGTGCC TGGAAGCAGA  
780  
GCGACTGAAG GGCTGCCTCA ACTCTGAGAA GATCTGCATC GCCCCTATCC TGGCTTGCCT  
840  
GCTCAGCCTC TGCCTCTGCA TTGCTGGCCT CAAGTGGGTC TTTGTGGACA AGATTTTGA  
900  
GTATGACTCT CCTACACACC TTGACCCTGG GAGGATAGGA CAAGACCCAA GGAGCACTGT  
960  
GGATCCTACA GCTCTGTCTG CCTGGGTGCC TTCGAGGTG TATGCCTCAC CCTTCCCCAT

1020  
ACCTAGCCTT GAGAGCAAGG CTGAAGTGAC AGTGCAAAC T GACAGCTCGC TCGTGCCCTC  
1080  
CAGGCCCTTC CTTGAGCCTT CTCTCTACAA CCGCATCCTA GATGTCGGGT TGTGGTCCTC  
1140  
TGCCACACCG TCACTGTCAC CATCCTCCCT GGAGCCTACC ACGGCATCTC AGGCACAAGC  
1200  
AACAGAAACC AATCTCCAAA CTGCTCCAAA ACTTTCCACT TCTACATCTA CAACTGGGAC  
1260  
AAGTCATCTC ACAAATGTG ACATAAAGCA GAAAGCCTTC TGTGTAAATG GGGGAGAGTG  
1320  
CTACATGGTT AAAGACCTCC CAAACCCTCC ACGATACCTA TGCAGGTGCC CAAATGAATT  
1380  
TACTGGTGAT CGCTGCCAAA ACTACGTAAT GGCCAGCTTC TACAAGCATC TTGGGATTGA  
1440  
ATTTATGGAA GCTGAGGAAC TGTACCAGAA ACGGGTGCTG ACCATAACTG GCATTTGCAT  
1500  
TGCTCTTCTA GTAGTTGGCA TCATGTGTGT GGTGGCCTAC TGCAAAACCA AGAAGCAGAG  
1560  
GAAAAAGTTG CATGACCGCC TTCGGCAGAG CCTTCGCTCA GAGAGGAACA ACGTTATGAA  
1620  
CATGGCAAAT GGGCCACACC ACCCAACCC ACCACCAGAC AATGTCCAGC TGGTGAATCA  
1680  
GTACGTTTCA AAAAACATAA TCTCCAGTGA ACGTGTCGTT GAGCGAGAAA CCGAGACCTC  
1740  
GTTTTCCACA AGCCACTACA CCTCAACAAC TCATCACTCC ATGACAGTCA CCCAGACGCC  
1800  
TAGCCACAGC TGGAGTAATG GCCATACCGA AAGCATTCTC TCCGAAAGCC ACTCCGTGCT  
1860  
CGTCAGCTCC TCAGTGGAGA ATAGCAGGCA CACCAGCCCA ACAGGGCCAC GAGGCCGCCT  
1920  
CAATGGCATT GGTGGGCCAA GGGAAGGCAA CAGCTTCCTC CGGCATGCAA GAGAGACCCC  
1980  
TGA CTCTAC CGAGACTCTC CTCACAGTGA AAGGTATGTC TCAGCTATGA CCACACCAGC  
2040

TCGCATGTCA CCCGTTGATT TCCACACTCC AACTTCTCCC AAGTCCCCTC CATCTGAAAT  
2100

GTCACCACCA GTTTCCAGCT TGACCATCTC CATCCCTTCG GTGGCGGTGA GTCCCTTTAT  
2160

GGACGAGGAG AGACCGCTGC TGTGTTGAC CCCACCACGG CTGGGTGAGA AGTACGACAA  
2220

CCACCTTCAG CAATTCAACT CCTTCCACAA CAATCCCACC CATGAGAGCA ACAGTCTGCC  
2280

ACCCAGTCCT CTGAGGATAG TGGAGGATGA AGAGTATGAG ACCACGCAGG AGTACGAACC  
2340

AGCACAGGAG CCTCCAAAGA AACTCACCAA CAGCCGAGG GTGAAAAGAA CAAAGCCCAA  
2400

TGGCCATATT TCCAGCAGGG TAGAAGTGGA CTCCGACACA AGCTCTCAGA GCACTAGCTC  
2460

TGAGAGCGAA ACAGAAGATG AAAGAATAGG TGAGGATACA CCATTTCTTA GCATACAAAA  
2520

TCCCATGGCA ACCAGTCTGG AGCCAGCCGC TGCATATCGG CTGGCTGAGA ACAGGACTAA  
2580

CCCGGCAAAT CGCTTCTCCA CACCAGAAGA GTTGCAAGCA AGGTTGTCCA GTGTAATAGC  
2640

TAACCAAGAC CCTATTGCTG TATAAGACAT AAACAAAACA CATAGATTCA CATGTAAAAC  
2700

TTTATTTTAT ATAATGAAGT ATTCCACCTT TAAATTAAAC AATTTATTTT ATTTTAGCAA  
2760

TTCCGCTGAT AGAAAACAAG AGTGGAAGAA GAAACTTTTA TAAATTAAGT ATACGTATGT  
2820

ACAAATGTGT TATGTGCCAT ATGTAGCAAT TTTTACAGT ATTTCCAAAA TGGGGAAAGA  
2880

TATCAATGGT GCCTTTATGT TATGTTATGT TGAGAGCAAG TTTTGTACAG CTACAATGAT  
2940

TGCTGTCCCG TAGTATTTTG CAAAACCTTC TAGCCCTCAG TTGTTCTGGC TTTTTTGTGC  
3000

ATTGCATTAT AATGACTGGA TGTATGATTT GCAAGAATTG CAGAAGTCCC CATTTGCTTG  
3060

TTGTGGAATC CCCAGATCAA AAAGCCCTGT TATGGCACTC ACACCCTATC CACTTCACCA

3120

GGAAAAAAAA AAAATCAAAA AAAAAAAAAA AAAAAAAGA AAAGAAAGAG AAAAAAGAAA  
3180

AGAAAAAGAA AAAAAAGCT GAAAAAATAA AA  
3212

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Arg	Gly	Cys	Cys	Cys	Tyr	Cys	His	Phe	Cys	Arg	Cys	Arg	Cys	Cys	Tyr
1					5					10					15
Xaa	Phe	Cys	Phe	Cys	Ser	Phe	Tyr	Arg	Met	Thr	Ile	Val	Phe	Leu	Ala
				20					25					30	
Leu	Ala	Asp	Thr	Ser	Leu	Arg	Cys	Ser	Arg	Xaa	Glu	Ser	Cys	Leu	Ser
				35					40					45	
Gly	Trp	Ala	Ile	Gly	Ser	Leu	Asn	Pro	Val	Asn	Leu	Phe	Ala	Ala	Arg
		50					55					60			
Leu	Cys	Leu	Ser	Pro	Arg	Pro	Pro	Ser	Pro	Cys	Phe	Val	Leu	Phe	Arg
	65					70				75					80
Leu	Leu	Ser	Gly	Gly	Arg	Ser	Phe	Pro	Gln	Ser	Glu	Glu	Leu	Glu	Leu
						85				90					95

Gln	Glu Arg Arg Ile Arg Asn Tyr Lys Ser Gly Gln Glu Thr Arg Ala	100	105	110
Arg	Xaa Leu Gln Ser Cys Pro Trp Leu Arg Gln Gly Ser Val Ser Gly	115	120	125
Ser	Gly Leu Gly Gln Gly Ala Gly Gly Leu Leu Phe Pro Val Arg Ser	130	135	140
Pro	Ser Pro Ser Ser Asp Asp Val Ala Val Ser Asp Leu Ser Leu Thr	145	150	155
Ser	Ala Leu Xaa Phe Leu Leu Ser Ala Val Thr Val Thr Pro Ser Leu	165	170	175
Gly	Val Cys Val Ser Gln Xaa Trp Thr Val Ile Glu Leu Arg Pro Phe	180	185	190
Thr	Gly Glu Leu Cys His Ser Xaa Cys Leu Asn Met Ser Glu Val Gly	195	200	205
Leu	Glu Thr Phe Pro Ser Pro Ser Ala Gln Leu Ser Pro Asp Ala Ser	210	215	220
Asp	Gly Gly Leu Pro Ala Glu Glu Asn Met Pro Gly Pro His Arg Glu	225	230	235
Cys	Ser Arg Val Pro Gly Val Ala Gly Leu Ala Ser Thr Cys Cys Val	245	250	255
Cys	Leu Glu Ala Glu Arg Leu Lys Gly Cys Leu Asn Ser Glu Lys Ile			

146

260 265 270

Ile Ala Pro Ile Leu Ala Cys Leu Leu Ser Leu Cys Leu Cys Ile  
Ala 275 280 285

Gly Leu Lys Trp Val Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser  
Pro 290 295 300

Thr His Leu Asp Pro Gly Arg Ile Gly Gln Asp Pro Arg Ser Thr  
Val 305 310 315  
320

Asp Pro Thr Ala Leu Ser Ala Trp Val Pro Ser Glu Val Tyr Ala  
Ser 325 330 335

Pro Phe Pro Ile Pro Ser Leu Glu Ser Lys Ala Glu Val Thr Val  
Gln 340 345 350

Thr Asp Ser Ser Leu Val Pro Ser Arg Pro Phe Leu Gln Pro Ser  
Leu 355 360 365

Tyr Asn Arg Ile Leu Asp Val Gly Leu Trp Ser Ser Ala Thr Pro  
Ser 370 375 380

Leu Ser Pro Ser Ser Leu Glu Pro Thr Thr Ala Ser Gln Ala Gln  
Ala 385 390 395  
400

Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser Thr  
Ser 405 410 415

Thr Thr Gly Thr Ser His Leu Thr Lys Cys Asp Ile Lys Gln Lys  
Ala 420 425 430

Asn	Phe Cys Val Asn Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro			
	435	440	445	
Arg	Pro Pro Arg Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp			
	450	455	460	
Glu	Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile			
480	465	470	475	
Thr	Phe Met Glu Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile			
	485	490	495	
Ala	Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val			
	500	505	510	
Arg	Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu			
	515	520	525	
Gly	Gln Ser Leu Arg Ser Glu Arg Asn Asn Val Met Asn Met Ala Asn			
	530	535	540	
Gln	Pro His His Pro Asn Pro Pro Pro Asp Asn Val Gln Leu Val Asn			
560	545	550	555	
Glu	Tyr Val Ser Lys Asn Ile Ile Ser Ser Glu Arg Val Val Glu Arg			
	565	570	575	
His	Thr Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Thr His			
	580	585	590	
His	Ser Met Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly			



595 600 605

Ser Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Leu Val Ser Ser  
610 615 620

Leu Val Glu Asn Ser Arg His Thr Ser Pro Thr Gly Pro Arg Gly Arg  
625 630 635

640

Ala Asn Gly Ile Gly Gly Pro Arg Glu Gly Asn Ser Phe Leu Arg His  
645 650 655

Tyr Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg  
660 665 670

His Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe  
675 680 685

Val Thr Pro Thr Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro  
690 695 700

Met Ser Ser Leu Thr Ile Ser Ile Pro Ser Val Ala Val Ser Pro Phe  
705 710 715

720

Glu Asp Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg  
725 730 735

Pro Lys Tyr Asp Asn His Leu Gln Gln Phe Asn Ser Phe His Asn Asn  
740 745 750

Glu Thr His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile Val  
755 760 765

Pro	Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu	770	775	780
Asn	Pro Lys Lys Leu Thr Asn Ser Arg Arg Val Lys Arg Thr Lys Pro	785	790	795
800				
Gln	Gly His Ile Ser Ser Arg Val Glu Val Asp Ser Asp Thr Ser Ser	805	810	815
Asp	Ser Thr Ser Ser Glu Ser Glu Thr Glu Asp Glu Arg Ile Gly Glu	820	825	830
Pro	Thr Pro Phe Leu Ser Ile Gln Asn Pro Met Ala Thr Ser Leu Glu	835	840	845
Arg	Ala Ala Ala Tyr Arg Leu Ala Glu Asn Arg Thr Asn Pro Ala Asn	850	855	860
Ala	Phe Ser Thr Pro Glu Glu Leu Gln Ala Arg Leu Ser Ser Val Ile	865	870	875
880				
Phe	Asn Gln Asp Pro Ile Ala Val Xaa Asp Ile Asn Lys Thr His Arg	885	890	895
Leu	Thr Cys Lys Thr Leu Phe Tyr Ile Met Lys Tyr Ser Thr Phe Lys	900	905	910
Trp	Asn Asn Leu Phe Tyr Phe Ser Asn Ser Ala Asp Arg Lys Gln Glu	915	920	925
Tyr	Lys Lys Lys Leu Leu Xaa Ile Lys Tyr Thr Tyr Val Gln Met Cys			

	930		935		940
	Val Pro Tyr Val Ala Ile Phe Tyr Ser Ile Ser Lys Met Gly Lys				
Asp	945		950		955
960	Ile Asn Gly Ala Phe Met Leu Cys Tyr Val Glu Ser Lys Phe Cys				
Thr		965		970	975
	Ala Thr Met Ile Ala Val Pro Xaa Tyr Phe Ala Lys Pro Ser Ser				
Pro		980		985	990
	Gln Leu Phe Trp Leu Phe Cys Ala Leu His Tyr Asn Asp Trp Met				
Tyr		995		1000	1005
	Asp Leu Gln Glu Leu Gln Lys Ser Pro Phe Ala Cys Cys Gly Ile				
Pro		1010		1015	1020
	Arg Ser Lys Ser Pro Val Met Ala Leu Thr Pro Tyr Pro Leu His				
Gln		1025		1030	1035
1040	Glu Lys Lys Lys Ile Lys Lys Lys Lys Lys Lys Lys Arg Lys Glu				
Arg		1045		1050	1055
	Glu Lys Arg Lys Glu Lys Glu Lys Lys Ser Xaa Lys Asn Lys				
		1060		1065	1070

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGCCTGTAA GATGCTGTAT CATTTGGTTG GGGGGGCCTC TCGTGGTAA TGGACCGTGA  
60  
GAGCGGCCAG GCCTTCTTCT GGAGGTGAGC CGATGGAGAT TTATTCCCCA GACATGTCTG  
120  
AGGTCGCCGC CGAGAGGTCC TCCAGCCCCT CCACTCAGCT GAGTGCAGAC CCATCTCTTG  
180  
ATGGGCTTCC GGCAGCAGAA GACATGCCAG AGCCCCAGAC TGAAGATGGG AGAACCCTG  
240  
GACTCGTGGG CCTGGCCGTG CCCTGCTGTG CGTGCCTAGA AGCTGAGCGC CTGAGAGGTT  
300  
GCCTCAACTC AGAGAAAATC TGCATTGTCC CCATCCTGGC TTGCCTGGTC AGCCTCTGCC  
360  
TCTGCATCGC CGGCCTCAAG TGGGTATTTG TGGACAAGAT CTTTGAATAT GACTCTCCTA  
420  
CTCACCTTGA CCCTGGGGGG TTAGGCCAGG ACCCTATTAT TTCTCTGGAC GCAACTGCTG  
480  
CCTCAGCTGT GTGGGTGTCG TCTGAGGCAT ACACTTCACC TGTCTCTAGG GCTCAATCTG  
540  
AAAGTGAGGT TCAAGTTACA GTGCAAGGTG ACAAGGCTGT TGTCTCCTTT GAACCATCAG  
600  
CGGCACCGAC ACCGAAGAAT CGTATTTTTG CCTTTTCTTT CTTGCCGTCC ACTGCGCCAT  
660  
CCTTCCCTTC ACCCACCCTG AACCCTGAGG TGAGAACGCC CAAGTCAGCA ACTCAGCCAC  
720  
AAACAACAGA AACTAATCTC CAAACTGCTC CTAAACTTTC TACATCTACA TCCACCACTG  
780  
GGACAAGCCA TCTTGTAATA TGTGCGGAGA AGGAGAAAAC TTTCTGTGTG AATGGAGGGG  
840  
AGTGCTTCAT GGTGAAAGAC CTTTCAAACC CCTCGAGATA CTTGTGCAAA GCGGAGGAG  
900  
CTGTACCAGA AGAGAGTGCT GACCATAACC GGCATCTGCA TCGCCCTCCT TGTGGTCGGC  
960  
ATCATGTGTG TGGTGGCCTA CTGCAAAACC AAGAAACAGC GAAAAAGCT GCATGACCGT  
1020

CTTCGGCAGA GCCTTCGGTC TGAACGAAAC AATACGATGA ACATTGCCAA TGGGCTCAC  
1080

CATCCTAACC CACCCCCCGA GAATGTCCAG CTGGTGAATC AATACGTATC TAAAAACGTC  
1140

ATCTCCAGTG AGCATATTGT TGAGAGAGAA GCAGAGACAT CCTTTTCCAC CAGTCACTAT  
1200

ACTTCCACAG CCCATCACTC CACTACTGTC ACCCAGACTC CTAGCCACAG CTGGAGCAAC  
1260

GGACACACTG AAAGCATCCT TTCCGAAAGC CACTCTGTAA TCGTGATGTC ATCCGTAGAA  
1320

AACAGTAGGC ACAGCAGCCC AACTGGGGCC G  
1351

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 449 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa	Ala	Cys	Lys	Met	Leu	Tyr	His	Leu	Val	Gly	Gly	Ala	Ser	Ala	Trp
	1				5					10					15
Glu	Trp	Thr	Val	Arg	Ala	Ala	Arg	Pro	Ser	Ser	Gly	Gly	Glu	Pro	Met
			20					25					30		
Ser	Ile	Tyr	Ser	Pro	Asp	Met	Ser	Glu	Val	Ala	Ala	Glu	Arg	Ser	Ser
			35				40					45			
Ala	Pro	Ser	Thr	Gln	Leu	Ser	Ala	Asp	Pro	Ser	Leu	Asp	Gly	Leu	Pro
	50						55					60			

Gly Ala Glu Asp Met Pro Glu Pro Gln Thr Glu Asp Gly Arg Thr Pro  
65 70 75 80

Arg Leu Val Gly Leu Ala Val Pro Cys Cys Ala Cys Leu Glu Ala Glu  
85 90 95

Leu Leu Arg Gly Cys Leu Asn Ser Glu Lys Ile Cys Ile Val Pro Ile  
100 105 110

Val Ala Cys Leu Val Ser Leu Cys Leu Cys Ile Ala Gly Leu Lys Trp  
115 120 125

Pro Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser Pro Thr His Leu Asp  
130 135 140

Ala Gly Gly Leu Gly Gln Asp Pro Ile Ile Ser Leu Asp Ala Thr Ala  
145 150 155

Arg Ser Ala Val Trp Val Ser Ser Glu Ala Tyr Thr Ser Pro Val Ser  
165 170 175

Ala Ala Gln Ser Glu Ser Glu Val Gln Val Thr Val Gln Gly Asp Lys  
180 185 190

Ile Val Val Ser Phe Glu Pro Ser Ala Ala Pro Thr Pro Lys Asn Arg  
195 200 205

Pro Phe Ala Phe Ser Phe Leu Pro Ser Thr Ala Pro Ser Phe Pro Ser  
210 215 220

Gln Thr Arg Asn Pro Glu Val Arg Thr Pro Lys Ser Ala Thr Gln Pro

225 230 235  
240 Thr Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser  
Thr 245 250 255  
Lys Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu  
260 265 270  
Ser Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu  
275 280 285  
Glu Asn Pro Ser Arg Tyr Leu Cys Lys Gly Gly Gly Ala Val Pro Glu  
290 295 300  
His Ser Ala Asp His Asn Arg His Leu His Arg Pro Pro Cys Gly Arg  
305 310 315  
320 His Val Cys Gly Gly Leu Leu Gln Asn Gln Glu Thr Ala Glu Lys  
Ala 325 330 335  
Asp Ala Xaa Pro Ser Ser Ala Glu Pro Ser Val Xaa Thr Lys Gln Tyr  
340 345 350  
Cys Glu His Cys Gln Trp Ala Ser Pro Ser Xaa Pro Thr Pro Arg Glu  
355 360 365  
Ala Pro Ala Gly Glu Ser Ile Arg Ile Xaa Lys Arg His Leu Gln Xaa  
370 375 380  
Tyr Tyr Cys Xaa Glu Arg Ser Arg Asp Ile Leu Phe His Gln Ser Leu  
385 390 395  
400

Gln Phe His Ser Pro Ser Leu His Tyr Cys His Pro Asp Ser Xaa Pro  
405 410 415

Cys Leu Glu Gln Arg Thr His Xaa Lys His Pro Phe Arg Lys Pro Leu  
420 425 430

Trp Asn Arg Asp Val Ile Arg Arg Lys Gln Xaa Ala Gln Gln Pro Asn  
435 440 445

Gly